# Evaluation of whole genome sequencing for routine subtyping of *Salmonella* Typhimurium for surveillance and outbreak investigation

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## CONTEXT

Subtyping = characterisation of bacterial isolates beyond the species and subspecies level

Why?
- Up-to-date diagnosis and surveillance of infectious diseases
- Outbreak: identify a link between the origin of the infection and the human isolate

Case study: *Salmonella enterica* subsp. *enterica* serovar Typhimurium (*S.* Typhimurium) and serovar 1,4,[5],12:i:- (*S.* 1,4,[5],12:i:-)

➡ important foodborne pathogen

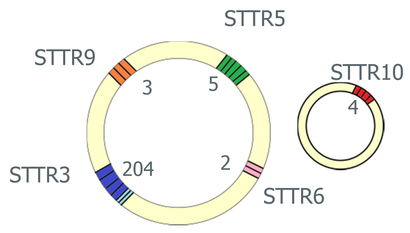
## CURRENT SITUATION @ BELGIAN NRC FOR SUBTYPING

### Phage typing

⊕ Very discriminative
Cheap

⊖ High level of expertise
NT and RDNC isolates

### MLVA

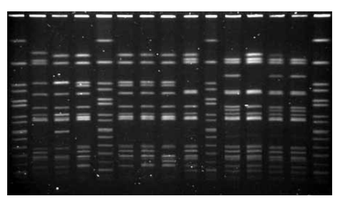



Profile: 3-5-2-4-204

⊕ Profiles easily compared between labs
Rapid

⊖ Too many profiles for surveillance
STTR5, STTR6, STTR10 not stable → outbreak?
(Wuyts *et al.*, 2013; Dimovski *et al.*, 2014)

### PFGE



⊕ Medium discriminative

⊖ Slow
Limited reproducibility

## IDEAL SITUATION @ BELGIAN NRC FOR SUBTYPING

Ideal subtyping method

- Highly discriminative
  Inexpensive
  Rapid
  Robust
- Universally applicable in epidemiology and diagnosis

? ➡ Whole genome sequencing

## ONGOING: EVALUATION OF WHOLE GENOME SEQUENCING FOR ROUTINE SUBTYPING

Human *S.* Typhimurium and *S.* 1,4,[5],12:i:- isolates

| Serovar | MLVA | Phage type DT104L | DT120 | DT138 | DT193 | RDNC |
|---|---|---|---|---|---|---|
| 1,4,[5],12:i:- | 3-12-10-NA-211 | - | 4 | - | 8 | - |
| | 3-12-11-NA-211 | - | 1 | 10 | - | 5 |
| | 3-13-11-NA-211 | - | - | 5 | 3 | 2 |
| | 3-14-11-NA-211 | - | - | - | 2 | - |
| Typhimurium | 3-12-10-NA-211 | - | 7 | 1 | 3 | - |
| | 3-12-11-NA-211 | - | 11 | - | 3 | 1 |
| | 3-13-11-NA-211 | - | 1 | - | - | - |
| | 3-14-11-NA-211 | - | - | - | - | 1 |
| | 3-14-18-14-311 | 1 | - | - | - | - |
| | 3-16-16-13-311 | 2 | - | - | - | - |

Outbreak-related → 7 isolates
3 (or 1) isolates → 7×3+1 = 22 isolates
} 29 isolates

➡ Data generation: next generation sequencing
- ➡ Illumina in outsourcing
  - Library type?
  - Coverage?

➡ Data analysis and interpretation
- Workflow: SNP- or allele-based?
- Definition of distinct subtype?
- Genotype – phenotype?
  - Antibiotic resistance
- Link with historical data?
  - Phage type – MLVA

➡ Universal subtyping method
- ➡ Other pathogens
  - *e.g. S.* Enteritidis

➡ Applicable in a routine setting?

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